

SEQUENCE LISTING

(1) GENERAL INFORMATION.

- (i) APPLICANT: Needleman, Philip  
Glenn, Kevin
- (ii) TITLE OF INVENTION: An Immunological Process and Constructs  
for Increasing the HDL Cholesterol Concentration by DNA  
Vaccination
- (iii) NUMBER OF SEQUENCES: 52
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Welsh & Katz, Ltd.
  - (B) STREET: 120 South Riverside Plaza, 22nd Floor
  - (C) CITY: Chicago
  - (D) STATE: IL
  - (E) COUNTRY: USA
  - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Gansch, Ph.D., Edward P.
  - (B) REGISTRATION NUMBER: 29,381
  - (C) REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (312) 655-1500
  - (B) TELEFAX: (312) 655-1501

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1446 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (viii) POSITION IN GENOME:
  - (C) UNITS: bp
- (x) PUBLICATION INFORMATION:
  - (A) AUTHORS: Drayna, Dennis  
Jannagin, Alisha Stephens  
McBean, John  
Henzel, William  
Kear, William  
Fielding, Christopher  
Lawn, Richard

(B) TITLE: Cloning and sequencing of human cholesteryl  
ester transfer protein cDNA  
(C) JOURNAL: Nature  
(D) VOLUME: 327  
(E) PAGES: 631-634  
(F) DATE: June 18-1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCTCCAAAG GACCTCGCA CAGGCAGGC ATCGTGTGCC GCATCACCAA GCCTGCCCTC	60
CTGGTGTGA ACCACGAGAC TCCCAAGGTC ATCCAGACCG CCTTCCAGCG AGCCAGCTAC	120
CCAGATATCA CCGGCGAGAA GGCATGATG CTCCTTGCC AAGTCAAGTA TGGGTTGCAC	180
AACATCCAGA CAGGCCATTC GTTCATCGCC AGCAGCCAGG TGGAGCTGGT GGAAGCCAAAG	240
TCCATTGATG TCTCCATCA GAADGTGTCT GTGGTCTTCA AGGGGACCCCT GAAGTATGGC	300
TACACCACTG CTTGGTGGCT GGTATTGAT CAGTCCATTG ACTTCGAGAT CGACTCTGCC	360
ATTACCTCC AGATCAACAC AATGTGACC TGTGACTCTG GTAGAGTGGC GACCGATGCC	420
CCCTACTGCT AACTGTCTTT TATAAGCTG CTCTGATC TCCAAGGGGA GCGAGAGCCT	480
GGGTGGATCA ACACCTGTT CACAAATTC ATCTCCTCA CCTGAAGCT GGTCTGAAG	540
GGACAGATCT GCAAGAGAT CAACCTCATC TCTAACATCA TGGCCGATT TGTCCAGACA	600
AGGCTGCCA GCATCTTTC AGATGAGAC ATTGGGGTGG ACATTTCCCT GACAGGTGAT	660
CCCTCATCA CAGCTCTCA CTTGAGTCC CATACAAGG GTCATTTCT CTACAAGAAAT	720
GTCACAGAG ACCCTGCTT CCGACCTTC TCGCCACAC TGCTGGGGGA CTCCTGGATG	780
CTGTACTTCT GCTTCTCTCA GCGATCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT	840
GGCTGCTCA TCTCAGCT CATGAGAGC GAGTTCAAGG CAGTGCTGGA GACCTGCGGC	900
TTCAACACCA ACAGGAAAT CTTCAGAG GGTGTGGCG GCTTCCCCAG CCAGGCCCAA	960
GTCACCGTCC ACTGCTCAA CATGCCAAG ATCTCCTGCC AAAACAAGG AGTCGTGCTC	1020
AATCTTCAG TATGCTGAA ATTCTCTTT CACGCCCAG ACCAGCAACA TTCTGTAGCT	1080
TACACATTG AACAGGATAT CGTACTACC CTCCAGGCCT CCTATTCTAA GAAAAAGCTC	1140
TTCTTAAGCC TCTTGATIT CAGATTACA CCAAGACTG TTTCCAACTT GACTGAGAGC	1200
AGCTCGAGT CATTACAGC CTCTGCA GCAATGATCA CCGCTGTGG CATCCCTGAG	1260
GTCATGTCT GCGCGAGCT AATTTTACA GCGCTCATGA ACAGCAAAG CGTGAGCTC	1320
TTCCACATCA TCAACCTCA GATTATCACT CAGATGGCT TCCTGCTGCT GCAGATGAC	1380
TTTGGCTTC CTACACCT GGTGGTGGAT TTCCTCAGA GCTTGAGCTA G	1431

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala Gln  
1 5 10 15  
Val Ala Val His  
2

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Ala Val Thr Phe Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val  
1 5 10 15  
Ala Tyr Arg Phe  
2

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp  
1 5 10 15  
Phe Leu Gln Ser Leu Ser  
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His Leu  
1 5 10 15  
Leu Asp Phe Gln  
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Leu Lys Gln  
1 5 10 15  
Leu Phe Thr Asn  
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu Gly Arg Val Lys Tyr  
1 5 10 15  
Gly Leu His Asn  
20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln  
1 5 10 15  
Val Thr Val His  
20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser Val  
1 5 10 15  
Ala Tyr Thr Phe  
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp  
1 5 10 15  
Phe Leu Gln Ser Leu Ser  
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu  
1 5 10 15  
Leu Asp Phe Gln  
20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Ile Lys Gln  
 1 5 10 15  
 Leu Phe Thr Asn  
 20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (E) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (I) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr  
 1 5 10 15  
 Gly Leu His Asn  
 20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (E) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (I) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
 (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAGGAAATCT TCCAGGAGCT TTCCAGAGGC CTTCACACCG GCCAGGCCCA GGTAGCCGTC 60  
 CAC 63

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (E) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (I) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
 (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGCCGTGA CGTCCGCTT CCCCCGCCCA GATGGCCGAG AAGCTGTGGC CTACAGGTTT 60

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 66 base pairs  
  (B) TYPE: nucleic acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
  (E) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGCTGCTGC AGATGACTT CCGTTTTCCC AAGCACCTGC TGGTGGATTT CCTGCAGAGC     60  
CTGAGC     66

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 60 base pairs  
  (B) TYPE: nucleic acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
  (E) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACCACCGTCC AGGCTTCTTA CTCCAGAAA AAGCTCTTCC TACACCTCTT GGATTTCAG     60

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 60 base pairs  
  (B) TYPE: nucleic acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
  (E) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCTCTGTC ACCTCCAGGG GGAGCGCGAG CCGGGGTGGC TCAAGCAGCT CTTCAAAAC     60

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
  - (1) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACGTCAGCG GCCAGAGGGC CGTGATGCTC CTCGGCCGGG TCAAGTACGG GCTGCACAAC 60

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
  - (1) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGGAAATCT TCCAAGAGGT TGTGGCGGC TTCCCAGCC AGGCCCAAGT CACCGTCCAC 60  
TGC 63

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
  - (1) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGATGGTGA AATTCTCTT TCCAGCCCA GACCAGCAAC ATTCTGTAGC TTACACATT 60



(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGCTGCTGC AGATGACTT TGGCTTCCT GAGCACCTGC TGGTGGATT CCTCCAGAGC 60  
TTGAGC 66

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACTACCGTCC AGGCTTCTA TTCTAAGAAA AAGCTCTCT TAAGCCTCTT GGATTTCAG 60

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGCTCTGC ATTCCCAAGG GGAGCGAGAG CCTGGGTGGA TCAAGCAGCT GTTCACAAAT 60

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATATCACCG GCGAGAAGGC CATGATGCTC CTTGGCCAAG TCAAGTATGG GTTGACACAAC 60

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 497 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Nagashima, M.  
McLean, J. W.  
Lawn, R. M.  
(B) TITLE: Cloning and mRNA tissue distribution of  
rabbit cholesteryl ester transfer protein  
(C) JOURNAL: J. Lipid Res.  
(D) VOLUME: 29  
(E) PAGES: 1643-1649  
(F) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala	Cys	Pro	Lys	Gly	Ala	Ser	Tyr	Glu	Ala	Gly	Ile	Val	Cys	Arg	Ile
1				5				10						15	
Thr	Lys	Pro	Ala	Leu	Leu	Val	Leu	Asn	Gln	Glu	Thr	Ala	Lys	Val	Val
			20					25					30		
Gln	Thr	Ala	Phe	Gln	Arg	Ala	Gly	Tyr	Pro	Asp	Val	Ser	Gly	Glu	Arg
			35				40					45			
Ala	Val	Met	Leu	Leu	Gly	Arg	Val	Lys	Tyr	Gly	Leu	His	Asn	Leu	Gln
			50			55					60				
Ile	Ser	His	Leu	Ser	Ile	Ala	Ser	Ser	Gln	Val	Glu	Leu	Val	Asp	Ala
65					70				75					80	
Lys	Thr	Ile	Asp	Val	Ala	Ile	Gln	Asn	Val	Ser	Val	Val	Phe	Lys	Gly
			85					90						95	
Thr	Leu	Asn	Tyr	Ser	Tyr	Thr	Ser	Ala	Trp	Gly	Leu	Gly	Ile	Asn	Gln
			100					105					110		
Ser	Val	Asp	Phe	Glu	Ile	Asp	Ser	Ala	Ile	Asp	Leu	Gln	Ile	Asn	Thr
			115				120					125			

Glu Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys  
130 135 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu  
145 150 155 160

Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu  
165 170 175

Lys Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser  
180 185 190

Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser  
195 200 205

Asp Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile  
210 215 220

Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys  
225 230 235 240

Asn Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu  
245 250 255

Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn  
260 265 270

Ser Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu  
275 280 285

Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr  
290 295 300

Asn Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln  
305 310 315 320

Ala Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln  
325 330 335

Asn Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe  
340 345 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp  
355 360 365

Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu  
370 375 380

His Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser  
385 390 395 400

Ser Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser  
405 410 415

Asn Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser  
420 425 430

Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val  
435 440 445

Ala Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile  
450 455 460

Ile Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met  
465 470 475 480

Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu  
485 490 495

Ser

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
 (C) UNITS: bp

(x) PUBLICATION INFORMATION:  
 (A) AUTHORS: Nagashima, Mariko  
 McLean, John W.  
 Lawn, Richard M.  
 (B) TITLE: Cloning and mRNA tissue distribution of  
 rabbit cholesteryl ester transfer protein  
 (C) JOURNAL: J. Lipid Res.  
 (D) VOLUME: 29  
 (E) PAGES: 1643-1649  
 (F) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCCTGTCCCA AAGGCGCTC CTACGAGGCT GGCATCGTGT GTCGCATCAC CAAGCGCGCC	60
CTCTTGGTGT TGAACCAAGA GACGGCCAAG GTGGTCCAGA CGGCCTTCCA GCGCGCTCGC	120
TATCCGGAAC TCAGCGCGCA GAGGGCCGTG ATGCTCCTCG GCCGGGTCAA GTACGGGCTG	180
CACAACCTCC AGATCAGCCA CTTGTCCATC GGCAGCAGCC AGGTGGAGGT GGTGGAGCGC	240
AAGACCATCC AGTGGGCCAT CCAGAACGTG TCCGTGGTCT TCAAGGGGAC CCTGAACTAC	300
AGCTACACCA GTGGCTGGGG GTTGGGCATC AATCAGTCTG TCGACTTCCA GATCGACTCT	360
GCCATTGACC TCAGATCAA CACAGAGCTG AACTGCGACG CTGGCAGTGT GCGCACCAAT	420
GCCCCCGAAT GTAGGTGGC TTTCCATAAA CTGCTCCTGC AACTCCAGGG GGAGCGCGAG	480
CCGGGGTGGC TCAGGAGCT GTTCACAAAC TTCATCTCTT TCACCCTGAA GCTGATTCTG	540
AAGCGAGAGG TTTCGAATGA GATCAACACC ATCTCCAACA TCATGGCTGA CTTTGTCCAG	600
ACGAGGGGCG CCAGCATCCT CTCAGATGGA GACATCGGGG TGGACATTTG CGTGACGGGG	660
GCCCTCTCCA TCAGAGCCAC CTACCTGGAG TCCATCACA AGGGTCACTT CACGCACAAG	720
AACGTCTCCG AGGCTTCCC CCTCCGGGCC TTCCCGCCCG GTCTTCTGGG GGAATCCCGC	780
ATGCTCTACT TTGGTTCTC CGATCAAGTG CTCAACTCCC TGGCCAGGCG CGCCTTCCAG	840
GAGGGCGCTC TCGTCTCAG CCTGACAGGG GATGAGTTCA AGAAAGTGT GAGAGCCAG	900
GGTTTCCACA CCAGCAGGA AATCTTCCAG GAGCTTTCCA GAGGCCTTCC CACCGGCCAG	960
GCCAGGATAG CCGTCTACTG CTTTAAGGTG CCAGAGATCT CTGCCAATA CCGGGGTGTC	1020
GTGGTGTCTT CTTTGTCTG CGTGACGTTT CGCTTCCCCG GCCCAGATGG CCGAGAAAGCT	1080
GTGGCCTACA GGTGTGAGGA GGATATCATC ACCACCGTCC AGGCCTCCTA CTCCCAAGAA	1140
AAGCTCTTCC TACGCTCTTT GGATTTCAG TCGTGGCCCG CCAGCGGAAG GGCAGGCAGC	1200

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TCAGCAAATC TCTCCGTGGC CCTCAGGACT GAGGCTAAGG CTGTTTCCAA CCTGACTGAG      1260
AGCCGCTCCG AGTCCCTGCA GAGCTCTCTC CGCTCCCTGA TCGCCACGGT GGGCATCCCG      1320
GAGGTATGCT CTCGCTCGA GGTGGCGTTC ACAGCCCTCA TGAACAGTAA AGGCCTGSAC      1380
CTCTTCGAAA TCATCAACCC CGAGATTATC ACTCTCGATG GCTGCCTGCT GCTGCAGATG      1440
GACTTCGGTT TTCGCAAGCA CCTGCTGGTG GATTTCCTGC AGAGCCTGAG CTAG              1494

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(2) INFORMATION FOR SEQ ID NO:28:

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 amino acids  
 (E) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (I) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(X) PUBLICATION INFORMATION:

(A) AUTHORS: Drayna, Dennis  
 Jarnagin, Alisha Stephens  
 McLean, John  
 Henzel, William  
 Kohr, William  
 Fielding, Christopher  
 Lawn, Richard  
 (E) TITLE: Cloning and sequencing of human cholesteryl  
 ester transfer protein cDNA  
 (C) JOURNAL: Nature  
 (V) VOLUME: 327  
 (P) PAGES: 632-634  
 (D) DATE: June 18-1987

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys Arg Ile Thr
 1           5           10           15
Lys Pro Ala Leu Leu Val Leu Asn His Glu Thr Ala Lys Val Ile Gln
 20           25           30
Thr Ala Phe Gln Arg Ala Ser Tyr Pro Asp Ile Thr Gly Glu Lys Ala
 35           40           45
Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile
 50           55           60
Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu Ala Lys
 65           70           75           80
Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr
 85           90           95
Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Trp Leu Gly Ile Asp Gln Ser
100          105          110
Ile Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln
115          120          125
Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys Tyr
130          135          140
Leu Ser Phe His Lys Leu Leu His Leu Gln Gly Glu Arg Glu Pro
145          150          155          160

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Gly Asp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys
      165                               170                               175

Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Val Ile Ser Asn
      180                               185                               190

Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
      195                               200                               205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr
      210                               215                               220

Ala Ser Tyr Leu Glu Ser His His Lys Gly His Phe Ile Tyr Lys Asn
      225                               230                               235                               240

Val Ser Gln Asp Leu Pro Leu Pro Thr Phe Ser Pro Thr Leu Leu Gly
      245                               250                               255

Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser
      260                               265                               270

Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser Leu Met
      275                               280                               285

Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr Asn
      290                               295                               300

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln
      305                               310                               315                               320

Val Thr Val His Cys Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys
      325                               330                               335

Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro Arg
      340                               345                               350

Pro Asp Gln Gln His Ser Val Ala Tyr Tyr Phe Glu Glu Asp Ile Val
      355                               360                               365

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu
      370                               375                               380

Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu Ser
      385                               390                               395                               400

Ser Ser Gln Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
      405                               410                               415

Gly Ile Ile Glu Val Met Ser Arg Leu Glu Val Val Phe Thr Ala Leu
      420                               425                               430

Met Asn Ser Lys Gly Val Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile
      435                               440                               445

Ile Thr Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe Pro
      450                               455                               460

Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
      465                               470                               475

```

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Swenson, T. L.  
et al.,  
(B) JOURNAL: J. Biol. Chem.  
(C) VOLUME: 264  
(E) PAGES: 14318-14326  
(G) DATE: 1989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His  
1 5 10 15  
Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Pape, Michael E.  
Rehberg, Edward F.  
Marotti, Keith R.  
Melchior, George W.  
(B) TITLE: Molecular Cloning, Sequence, and Expression  
of Cynomolgus Monkey Cholesteryl Ester Transfer  
Protein  
(C) JOURNAL: Arteriosclerosis and Thrombosis  
(D) VOLUME: 11  
(E) ISSUE: 6  
(F) PAGES: 1759-1771  
(G) DATE: Nov/Dec-1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Leu Ala Ala Thr Val Leu Thr Leu Ala Leu Leu Gly Asn Val His  
1 5 10 15  
Ala Cys Ser Lys Gly Thr Ser His Lys Ala Gly Ile Val Cys Arg Ile  
20 25 30  
Thr Lys Phe Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Ile  
35 40 45  
Gln Ser Ala Phe Gln Arg Ala Asn Tyr Pro Asn Ile Thr Gly Glu Lys  
50 55 60  
Ala Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln  
65 70 75 80  
Ile Ser His Leu Ser Ile Ala Ser Ser Arg Val Glu Leu Val Glu Ala  
85 90 95  
Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly  
100 105 110  
Thr Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Gly Leu Gly Ile Asp Gln  
115 120 125

Ser Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr  
130 135 140

Gln Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys  
145 150 155 160

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu  
165 170 175

Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu  
180 195 190

Lys Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Ile Ile Ser  
195 200 205

Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser  
210 215 220

Asp Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Ile Ile  
225 230 235 240

Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly Tyr Phe Ile Tyr Lys  
245 250 255

Asn Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Ala Leu Leu  
260 265 270

Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Gln Val Phe His  
275 280 285

Ser Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Thr Leu Ser Leu  
290 295 300

Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr  
305 310 315 320

Asn Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala  
325 330 335

Gln Val Thr Val His Cys Leu Lys Met Pro Arg Ile Ser Cys Gln Asn  
340 345 350

Lys Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro  
355 360 365

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp Ile  
370 375 380

Met Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser  
385 390 395 400

Leu Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu  
405 410 415

Ser Ser Ser Glu Ser Val Gln Ser Phe Leu Gln Ser Met Ile Thr Thr  
420 425 430

Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Ala Val Phe Thr Ala  
435 440 445

Leu Met Asn Ser Lys Gly Leu Ser Leu Phe Asp Ile Ile Asn Pro Glu  
450 455 460

Ile Ile Thr Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe  
465 470 475 480

Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
485 490



(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Pape, Michael E.  
Rehberg, Edward F.  
Marotti, Keith R.  
Melchior, George W.
- (B) TITLE: Molecular Cloning, Sequence, and Expression  
of Cynomolgus Monkey Cholesteryl Ester Transfer  
Protein
- (C) JOURNAL: Arteriosclerosis and Thrombosis
- (D) VOLUME: 11
- (E) ISSUE: 6
- (F) PAGES: 1759-1771
- (G) DATE: Nov/Dec-1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCTGGCTG CCAGGCTCCT GACCGTGGCC CTGCTGGGCA ATGTCCACCC CTGCTCCAAA	60
GGTAGCTCAC ACAAGGCAGG CATTGTGTGC CGCATCACCA AGCGTGCCTT CTGCTGTGTG	120
AACCAACAGA CTGCTCAAGT GATCCAGTCT GCGTTCAGC GAGCCAACTA CCCAAATATC	180
ACAGGCGAGA AGGCGATGAT GCTCCTTGGC CAAGTCAAGT ATGGGTTGCA CAACATCCAA	240
ATCAGCCACT TGTCCATCGC CAGCAGCCGG GTGGAGCTGG TGAAGCCAA GTCCATTGAT	300
GTCTCCATTC AGAGGTGTC TGTGTCTTC AAGGGGACCC TGAAGTATGG CTACAGCACT	360
GCCTGGGGGC TGGGCAATGA TCAGTCCCTT GACTTCGAGA TCGACTCTGC CATTGACCTC	420
CAGATCAACA CACCACTGAC CTGTGACTCT GGTAGAGTGA GGACTGATGC CCTGACTGTC	480
TACCTGTCTT TCCCTAAGCT GCTCCTGAT CTCCAAGGGG AGCGAGAGCC CGGGTGGATC	540
AAGCACTGTG TCACTAAGTT CATCTCCTTC ACCCTGAAGC TGGTCTGAA GGGACAGATC	600
TGCAAGAGA TCAAGATCAT CTCCAACATC ATGGCCGATT TTGTCCAGAC AAGGGCTGCC	660
AGTATCTTT CAGATGGAGA CATCTGGGTG GACATTTCCC TGACAGGTGA TCCCATCATT	720
ACAGCTCCTT ACCCTGATTC CCATCACAAG GGTATTTC A TCTATAAGAA TGTCTCGGAG	780
GACCTCCAC TCCCTACCTT CTCGCCCCCA CTGCTGGGGG ACTCCCGCAT GCTGTACTTC	840
TGGTTCTCCG AGCAAGTCTT CCACTCCTTG GCCAAGGTAG CTTTCCAAGA TGCCTGCTC	900
ACGCTCAGCC TGATGGGAGA CGAGTTCAAG GCAGTGTGTA AGACTTGAGG CTTCAACACC	960
AACCAAGAAA TCTCTAAGA GGTCTCTGTC GCGTTCCTCA GCCAGGCCCA AGTCAAGCTC	1020
CACTCCTCA AGAGGCGAG GATCTCTGTC CAAAACAAGG GAGTCTGCTT CAATTCTTCG	1080
GTGATGTTGA AATCTCTCTT TCCAGCTCA BACCAGCAAC ACTCTGTAGC TTACACATTT	1140
GAAGAGGATA TCAAGACAC CGTCCAGGTC TCCTATTCTA AAAAAAGCT CTTCTTAAGC	1200
CTCTTGATT TCCATATTAC ACCAAAGACT GTTTCCAACT TGAAGTGAAG CAGCTCAG	1260

TCCGTCCAGA GCTTCTTCA GTCAATGATC ACCACTGTGG GCATCCCTGA GGTCAATGTCT 1320  
 CGGCTTGAGG CAGTGTTTAC AGCCCTCATG AACAGCAAAG GCCTGAGCCT CTTGACATC 1380  
 ATCAATCCTG AGATTATCAC TCGAGATGGC TTCCTGCTGC TGCAGATGGA CTTTGGCTTC 1440  
 CCTGAGCACC TGCTGGTBSA TTCTCTCCAG AGCTTGAGCT AGAAGTCTTC AAGGACGTCA 1500  
 GGATGGGG 1508

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln  
 1 5 10 15  
 Val Thr Val His  
 20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser Val  
 1 5 10 15  
 Ala Tyr Thr Phe  
 20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp  
 1 5 10 15

Phe Leu Gln Ser Leu Ser

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu  
1 5 10 15

Leu Asp Phe Gln  
20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Ile Lys Gln  
1 5 10 15

Leu Phe Thr Asn  
20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asn Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr  
1 5 10 15

Gly Leu His Asn  
20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 183 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1         5         10         15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20         25         30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35         40         45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50         55         60
Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65         70         75         80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
 85         90         95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100        105        110
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115        120        125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130        135        140
Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145        150        155        160
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165        170        175
Gln Ser Arg Glu Ser Gln Cys
180

```

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 552 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

ATGGACATCG ACCCTATAA AGAATTGGA GCTACTGTGG AGTTACTCTC GTTTTTCCT      60
TCTGACTTCT TTCCTTCAGT ACGAGATCTT CTAGATACCG CCTCAGCTCT GTATCGGGAA      120

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GCCTTAGAGT CTCCTGAGCA TTGTTACCT CACCATACTG CACTCAGGCA AGCAATTCTT      180
TGCTGGGGGG AACTAATGAC TCTAGCTACC TGGGTGGGTG TTAATTTGGA AGATCCAGCG      240
TCTAGAGACC TAGTAGTCAE TTATGTCAAC ACTAATATGG GCCTAAAGTT CAGGCAACTC      300
TTGTGGTTTC ACATTTCTTJ TCTCACTTTT GGAAGAGAAA CAGTTATAGA GTATTTGGTG      360
TCTTTCGGAG TGTGATTCE CACTCCTCCA GCTTATAGAC CACCAAATGC CCCTATCCTA      420
TCAACACTTC CGGAGACTAC TGTTGTTAGA CGACGAGGCA GGTCCCCTAG AAGAAGAACT      480
CCCTCGCCTC GCAGACGAAG GTCTCAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGGAA      540
TCTCAATGTT AG                                                              552

```

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val
1           5           10           15
Val Ser Tyr Val Asn Thr Asn Met Gly
                20           25

```

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
1           5           10           15
Ile Glu Tyr Leu Val
                20

```

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro  
1 5 10 15  
Asn Ala Pro Ile Leu  
21

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATCCCATGG ACATCGACCG TTATAAAGAA TTTGG

35

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCAAGCTT TTAACATGGA GATTCGCGAG ATTGAGATCT TCTG

44

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:  
GATCGAATTC ACTAGTTGGA AGATCCAGCG TCTAGAGACC TAG 43

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:  
GATCGAATTC CTCGAGCTAG AGTCATTAGT TCCCCCAGC A 41

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:  
GATTATCACT CGAGATGGGT TCCTGCTGCT GCAG 34

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:  
GATCGAATTC AGTGGTCAAG CTCTGGAGGA AATCCACCAG 40

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His  
1 5 10 15  
Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGCCGCAACG TTCTACTAGC TCAGGCTCTG CAGGAAATCC ACCAGCAGGT G 51

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGCCGCCCAT GGCTGTCTCC AAAGGCGCCT CCTACGAGGC T 41